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RAW SEQUENCE LISTING

DATE: 04/04/2002

PATENT APPLICATION: US/09/101,518A

TIME: 15:46:42

Input Set : A:\PF218US substitute sequence listing.txt

Output Set: N:\CRF3\04042002\I101518A.raw

C--> 3 <110> APPLICANT: Li, Yi
 5 <120> TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
 7 <130> FILE REFERENCE: PF218US
 9 <140> CURRENT APPLICATION NUMBER: US 09/101,518A
 10 <141> CURRENT FILING DATE: 2002-03-18
 12 <150> PRIOR APPLICATION NUMBER: PCT/US96/00499
 13 <151> PRIOR FILING DATE: 1996-01-11
 15 <160> NUMBER OF SEQ ID NOS: 9
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1876
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (173)..(1420)
 27 <223> OTHER INFORMATION:
 30 <400> SEQUENCE: 1
 31 cctgaagggga gagcagggag agagaggaca gtggccagag agggctctgg gcactggagg 60
 33 gacgctcttc ttctgcca ggggtccctg ggccgatggg atcacgcaga agaatgcgag 120
 35 agaagcagcc ttgagaagg gaagtcacta tcccagagcc cagactgagc gg atg gag 178
 36 Met Glu
 37 1
 39 ttg agg aag tac ggc cct gga aga ctg gcg ggg aca gtt ata gga gga 226
 40 Leu Arg Lys Tyr Gly Pro Gly Arg Leu Ala Gly Thr Val Ile Gly Gly
 41 5 10 15
 43 gct gct cag agt aaa tca cag act aaa tca gac tca atc aca aaa gag 274
 44 Ala Ala Gln Ser Lys Ser Gln Thr Lys Ser Asp Ser Ile Thr Lys Glu
 45 20 25 30
 47 ttc ctg cca ggc ctt tac aca gcc cct tcc tcc ccg ttc ccg ccc tca 322
 48 Phe Leu Pro Gly Leu Tyr Thr Ala Pro Ser Ser Pro Phe Pro Pro Ser
 49 35 40 45 50
 51 cag gtg agt gac cac caa gtg cta aat gac gcc gag gtt gcc gcc ctc 370
 52 Gln Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val Ala Ala Leu
 53 55 60 65
 55 ctg gag aac ttc agc tct tcc tat gac tat gga gaa aac gag agt gac 418
 56 Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn Glu Ser Asp
 57 70 75 80
 59 tcg tgc tgt acc tcc ccg ccc tgc cca cag gac ttc agc ctg aac ttc 466
 60 Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser Leu Asn Phe
 61 85 90 95
 63 gac cgg gcc ttc ctg cca gcc ctc tac agc ctc ctc ttt ctg ctg ggg 514
 64 Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe Leu Leu Gly

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65	100	105	110	
67	ctg ctg ggc aac ggc gcg gtg gca gcc gtg ctg ctg agc cgg cgg aca	562		
68	Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu Leu Ser Arg Arg Thr			
69	115 120 125 130			
71	gcc ctg agc agc acc gac acc ttc ctg ctc cac cta gct gta gca gac	610		
72	Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala Val Ala Asp			
73	135 140 145			
75	acg ctg ctg gtg ctg aca ctg ccg ctc tgg gca gtg gac gct gcc gtc	658		
76	Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp Ala Ala Val			
77	150 155 160			
79	cag tgg gtc ttt ggc tct ggc ctc tgc aaa gtg gca ggt gcc ctc ttc	706		
80	Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly Ala Leu Phe			
81	165 170 175			
83	aac atc aac ttc tac gca gga gcc ctc ctg ctg gcc tgc atc agc ttt	754		
84	Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu Ala Cys Ile Ser Phe			
85	180 185 190			
87	gac cgc tac ctg aac ata gtt cat gcc acc cag ctc tac cgc cgg ggg	802		
88	Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr Arg Arg Gly			
89	195 200 205 210			
91	ccc ccg gcc cgc gtg acc ctc acc tgc ctg gct gtc tgg ggg ctc tgc	850		
92	Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp Gly Leu Cys			
93	215 220 225			
95	ctg ctt ttc gcc ctc cca gac ttc atc ttc ctg tcg gcc cac cac gac	898		
96	Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala His His Asp			
97	230 235 240			
99	gag cgc ctc aac gcc acc cac tgc caa tac aac ttc cca cag gtg ggc	946		
100	Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro Gln Val Gly			
101	245 250 255			
103	cgc acg gct ctg cgg gtg ctg cag ctg gtg gct ggc ttt ctg ctg ccc	994		
104	Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe Leu Leu Pro			
105	260 265 270			
107	ctg ctg gtc atg gcc tac tgc tat gcc cac atc ctg gcc gtg ctg ctg	1042		
108	Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala Val Leu Leu			
109	275 280 285 290			
111	gtt tcc agg ggc cag cgg cgc ctg cgg gcc atg cgg ctg gtg gtg gtg	1090		
112	Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu Val Val Val			
113	295 300 305			
115	gtc gtg gtg gcc ttt gcc ctc tgc tgg acc ccc tat cac ctg gtg gtg	1138		
116	Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His Leu Val Val			
117	310 315 320			
119	ctg gtg gac atc ctc atg gac ctg ggc gct ttg gcc cgc aac tgt ggc	1186		
120	Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg Asn Cys Gly			
121	325 330 335			
123	cga gaa agc agg gta gac gtg gcc aag tcg gtc acc tca ggc ctg ggc	1234		
124	Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser Gly Leu Gly			
125	340 345 350			
127	tac atg cac tgc tgc ctc aac ccg ctg ctc tat gcc ttt gta ggg gtc	1282		
128	Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe Val Gly Val			
129	355 360 365 370			

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131 aag ttc cgg gag cgg atg tgg atg ctg ctc ttg cgc ctg ggc tgc ccc      1330
132 Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu Gly Cys Pro
133                               375                               380                               385
135 aac cag aga ggg ctc cag agg cag cca tcg tct tcc cgc cgg gat tca      1378
136 Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg Arg Asp Ser
137                               390                               395                               400
139 tcc tgg tct gag acc tca gag gcc tcc tac tcg ggc ttg tga      1420
140 Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu
141                               405                               410                               415
143 ggccggaatc cgggctcccc tttcgcccac agtctgactt ccccgcatc caggctcctc      1480
145 cctccctctg ccggctctgg ctctcccaa tctcctcgct cccgggactc actggcagcc      1540
147 ccagcaccac cagggtctccc gggaagccac cctccagct ctgaggactg caccattgct      1600
149 gctccttagc tgccaagccc catcctgccg cccgaggtgg ctgcctggag cccactgcc      1660
151 cttctcatctt ggaaactaaa acttcatctt cccaagtgc ggggagtaca aggcattggcg      1720
153 tagaggggtgc tgccccatga agccacagcc caggcctcca gctcagcagt gactgtggcc      1780
155 atggtcccca agacctctat atttggcttt ttatttttat gtctaaaatc ctgcttaaaa      1840
157 cttttcaata aacaagatcg tcaggaaaaa aaaaaa      1876
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 415
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 2
167 Met Glu Leu Arg Lys Tyr Gly Pro Gly Arg Leu Ala Gly Thr Val Ile
168 1 5 10 15
171 Gly Gly Ala Ala Gln Ser Lys Ser Gln Thr Lys Ser Asp Ser Ile Thr
172 20 25 30
175 Lys Glu Phe Leu Pro Gly Leu Tyr Thr Ala Pro Ser Ser Pro Phe Pro
176 35 40 45
179 Pro Ser Gln Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val Ala
180 50 55 60
183 Ala Leu Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn Glu
184 65 70 75 80
187 Ser Asp Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser Leu
188 85 90 95
191 Asn Phe Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe Leu
192 100 105 110
195 Leu Gly Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu Leu Ser Arg
196 115 120 125
199 Arg Thr Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala Val
200 130 135 140
203 Ala Asp Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp Ala
204 145 150 155 160
207 Ala Val Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly Ala
208 165 170 175
211 Leu Phe Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu Ala Cys Ile
212 180 185 190
215 Ser Phe Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr Arg
216 195 200 205
219 Arg Gly Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp Gly

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220      210      215      220
223 Leu Cys Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala His
224 225      230      235      240
227 His Asp Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro Gln
228      245      250      255
231 Val Gly Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe Leu
232      260      265      270
235 Leu Pro Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala Val
236      275      280      285
239 Leu Leu Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu Val
240      290      295      300
243 Val Val Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His Leu
244 305      310      315      320
247 Val Val Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg Asn
248      325      330      335
251 Cys Gly Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser Gly
252      340      345      350
255 Leu Gly Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe Val
256      355      360      365
259 Gly Val Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu Gly
260      370      375      380
263 Cys Pro Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg Arg
264 385      390      395      400
267 Asp Ser Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu
268      405      410      415
271 <210> SEQ ID NO: 3
272 <211> LENGTH: 29
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: Contains a BamHI restriction enzyme site
279 <400> SEQUENCE: 3
280 cgggatcctc catggagttg aggaagtac 29
283 <210> SEQ ID NO: 4
284 <211> LENGTH: 30
285 <212> TYPE: DNA
286 <213> ORGANISM: Artificial sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Contains complementary sequences to a BamHI site
291 <400> SEQUENCE: 4
292 ggcggatccc gtcacaagc ccgagtagga 30
295 <210> SEQ ID NO: 5
296 <211> LENGTH: 34
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Contains a HindIII site
303 <400> SEQUENCE: 5
304 gtccaagctt gccaccatgg agttgaggaa gtac 34

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307 <210> SEQ ID NO: 6
308 <211> LENGTH: 57
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Contains complementary sequences to a XhoI site, translation
stop
314      codon, and an HA tag
316 <400> SEQUENCE: 6
317 ctgctcgagt caagcgtagt ctgggacgtc gtatgggtag cacaagcccg agtagga      57
320 <210> SEQ ID NO: 7
321 <211> LENGTH: 31
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Contains a BamHI restriction enzyme site followed by 5
nucleotide
327      s resembling an efficient signal for the initiation of translatio
328      n in eukaryotic cells (J. Mol. Biol. 1987, 196, 947-950, Kozak, M
329      .)
331 <400> SEQUENCE: 7
332 cgggatccct cccatggagt tgaggaagta c      31
335 <210> SEQ ID NO: 8
336 <211> LENGTH: 29
337 <212> TYPE: DNA
338 <213> ORGANISM: Artificial sequence
340 <220> FEATURE:
341 <223> OTHER INFORMATION: Contains the cleavage site for the restriction endonuclease
BamHI
343 <400> SEQUENCE: 8
344 cgggatcccg ctcacaagcc cgagtagga      29
347 <210> SEQ ID NO: 9
348 <211> LENGTH: 353
349 <212> TYPE: PRT
350 <213> ORGANISM: Homo sapiens
352 <400> SEQUENCE: 9
354 Glu Ser Asp Ser Phe Glu Asp Phe Trp Lys Gly Glu Asp Leu Ser Asn
355 1      5      10      15
358 Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe Leu Leu Asp Ala Ala Pro
359      20      25      30
362 Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys Tyr Phe Val Val Ile Ile
363      35      40      45
366 Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val Met
367      50      55      60
370 Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr
371 65      70      75      80
374 Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu Pro
375      85      90      95
378 Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe Leu
379      100     105     110
382 Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile
383      115     120     125

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VERIFICATION SUMMARY DATE: 04/04/2002
PATENT APPLICATION: US/09/101,518A TIME: 15:46:43

Input Set : A:\PF218US substitute sequence listing.txt
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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date